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JUN 22 2007

Listing of the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) A method for determining a haplotype of a subject comprising the steps of:
   - (a) diluting a nucleic acid sample from the subject into a single molecule dilution;
   - (b) amplifying the diluted single molecule dilution [[and]] in a multiplex amplification reaction with at least [[two]] four different primer pairs designed to amplify at least [[two]] four nucleic acid regions each comprising at least [[two]] one polymorphic site[[s]] ~~in the nucleic acid template~~;
   - (c) genotyping the at least [[two]] four nucleic acid regions ~~that~~ wherein each region contains at least one polymorphic site ~~in the single nucleic acid molecule~~ wherein the genotyping is performed using primer extension and mass spectrometric detection; [[and]]
   - (d) repeating steps a-c from the same nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas to determine the haplotype; and
   - [[(d)]] (e) determining the haplotype from the genotypes of the at least [[the]] [[two]] four polymorphic sites to obtain a haplotype for the subject.
2. (Cancelled)
3. (Currently amended) The method of claim [[2]] 1, further comprising comparing the haplotype with a haplotype from a control or a database of haplotypes from controls to determine association of the haplotype with a biological trait.
4. (Currently amended) The method of claim 1, wherein the at least [[two]] four polymorphic sites contain a polymorphism that is a single nucleotide polymorphism.

5. (Currently amended) The method of claim 1, wherein the ~~polymorphism is~~ at least four polymorphic sites contain a polymorphism selected from a deletion, an insertion, a substitution or an inversion.

6. (Currently amended) The method of claim 1, wherein the at least [[two]] four polymorphic sites contain a polymorphism ~~that is a combination~~ wherein each of the polymorphisms is ~~of one or more markers~~ selected from the group consisting of a single nucleotide polymorphism, deletion, an insertion, a substitution or an inversion.

7. (Cancelled)

8. (Cancelled)

9. (Currently amended) A method of diagnosing a disease condition or disease susceptibility by determining a disease related haplotype in a subject comprising the steps of:

(a) diluting a nucleic acid sample from the subject into a single molecule dilution;

(b) amplifying the diluted single molecule dilution [[and]] in a multiplex amplification reaction with at least two primer pairs designed to amplify a region comprising at least two polymorphic sites in the nucleic acid template;

(c) genotyping the polymorphic sites in the single nucleic acid molecule wherein the genotyping is performed using primer extension and mass spectrometric detection;

(d) repeating steps a-c from the same nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas to determine the haplotype;

[[(d)]] (e) determining the haplotype from the genotype of at least two polymorphic sites to obtain a haplotype for the subject; and

[[(e)]] (f) comparing the haplotype of the subject to known disease-associated haplotypes, wherein a match in the sample haplotype with a

disease-associated haplotype indicates that the subject has the disease or that the subject is susceptible for the disease.

10. (Cancelled)

11. (Cancelled)

12. (Currently amended) A method of determining a haplotype of a subject comprising the steps of:

(a) treating a nucleic acid sample from the subject with a composition that differentially affects an epigenetically modified nucleotide in the nucleic acid sample to effectively create polymorphisms based on the epigenetic modification;

(b) diluting the treated nucleic acid sample into a single copy dilution;

(c) amplifying the diluted nucleic acid sample using at least [[two]] four different primer pairs in a multiplex amplification reaction;

(d) genotyping the amplified sample, wherein genotyping is performed using primer extension and mass spectrometric detection; [[and]]

(e) repeating steps b-c from the same treated nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas; and

[[(e)]] (f) determining the haplotype of the subject from the genotyped sample.

13. (Cancelled)

14. (Cancelled)

15. (Original) The method of claim 12, wherein the epigenetically modified nucleotide is a methylated nucleotide.

16. (Original) The method of claim 15, wherein the nucleic acid sample is treated with bisulfite.

17. (Currently amended) A method of determining a haplotype in a subject comprising the steps of:

(a) digesting a nucleic acid sample from the subject with a methylation-sensitive restriction enzyme so that either unmethylated DNA or methylated DNA is left intact, depending on which enzyme is used;

(b) diluting the digested nucleic acid sample to a single molecule concentration;

(c) amplifying the diluted and undiluted nucleic acid sample with at least two different primer pairs in a multiplex amplification reaction;

(d) genotyping the amplified samples, wherein genotyping is performed using primer extension and mass spectrometric detection;; [[and]]

(e) repeating steps b-c from the same treated nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas; and

[[(e)]] (f) determining a haplotype of a methylated nucleic acid wherein at least one polymorphic marker next to the methylation site, together with the methylation site, constitutes a haplotype.

18. (Cancelled)

19. (Cancelled)